



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 108425

TO: Terra Gibbs
Location: CM1/12A12/11E12
Art Unit: 1635
Monday, November 17, 2003

Case Serial Number: 10/008789

From: David Schreiber
Location: Biotech-Chem Library
CM1-6A03
Phone: 308-4292

david.schreiber@uspto.gov

Search Notes

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____

Art Unit: _____ Phone Number 30 _____ Serial Number: _____

Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:	<u>D. Schreber</u>	NA Sequence (#): <u>6</u>	STN _____
Searcher Phone #:	<u>308-4292</u>	AA Sequence (#): _____	Dialog _____
Searcher Location:	<u>Car 1 6A03</u>	Structure (#): _____	Questel Orbit: _____
Date Searcher Prepped:	_____	Bibliographic: _____	OrLink: _____
Date Completed:	<u>11/17</u>	Ligation: _____	Lexis/Nexis: _____
Searcher Prep & Review Time:	<u>13</u>	Fulltext: _____	Sequence Systems: <u>Compugen, plus-excel, and Grou</u>
Clerical Prep Time:	_____	Patent Family: _____	WWW Internet: _____
Review Time:	<u>205</u>	Other: _____	Other (specify): _____

108425

Schreiber, David

From: Gibbs, Terra 79523
Sent: Tuesday, November 04, 2003 2:02 PM
To: Schreiber, David
Subject: Sequence search request...

Hi David,

Doug Schultz and Karen LaCourcicie recommended that I send you this search request.

I have a request for a score over length search:

I need a length limited nucleotide sequence search against SEQ ID NO:22 of USSN 10/008,789, where the returns are rank ordered based on the score over length/ratio as we've discussed. I need the lengths limited to hits between 8 and 30 nucleotides, and I'll take as many hits as you can import into excel (64,000?), and alignments for anything above .75 on the above ratio. Hope this is clear, please call me if it's not. I do not need the interference databases searched.

Thanks!

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
CM1, 12A12
703-306-3221

1	18.5	
34	24.5	
38	25	4
4	13.5	15.5



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

- I am an examiner in Workgroup: Example: 1610
- Relevant prior art **found**, search results used as follows:
- 102 rejection
 - 103 rejection
 - Cited as being of interest.
 - Helped examiner better understand the invention.
 - Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 14:05:38 ; Search time 1559 Seconds
(without alignments)
524.819 Million cell updates/sec

Title: US-10-008-789-22

Perfect score: 20

Sequence: 1 gcttcaggagcccggtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 1007914

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65000 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*

20: em_om:*

 21: em_or:*

 22: em_ov:*

 23: em_pat:*

 24: em_ph:*

 25: em_pl:*

 26: em_ro:*

 27: em_sts:*

 28: em_un:*

 29: em_vi:*

 30: em_htg_hum:*

 31: em_htg_inv:*

 32: em_htg_other:*

 33: em_htg_mus:*

 34: em_htg_pln:*

 35: em_htg_rod:*

 36: em_htg_mam:*

 37: em_htg_vrt:*

 38: em_sy:*

 39: em_htgo_hum:*

 40: em_htgo_mus:*

 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query				Score/Length
	Score	Match	Length	DB ID	
2765	9	45	10	6 AX152921	0.9
2766	9	45	10	6 AX538718	0.9
c10209	8	40	9	6 AX009053	0.888889
c1514	9.4	47	11	6 AX623720	0.854545
1515	9.4	47	11	6 AX630279	0.854545
c1516	9.4	47	11	6 AX631141	0.854545
5998	8.4	42	10	6 AX152864	0.84
5999	8.4	42	10	6 AX152865	0.84
6000	8.4	42	10	6 BD007939	0.84
6001	8.4	42	10	6 BD083228	0.84
20689	7.4	37	9	6 AX668683	0.822222
20690	7.4	37	9	6 AX668684	0.822222
20691	7.4	37	9	6 AX668685	0.822222
20692	7.4	37	9	6 AX668686	0.822222
20693	7.4	37	9	6 E12006	0.822222
c2767	9	45	11	6 AX098793	0.818182
2768	9	45	11	6 AX098794	0.818182

c2769	9	45	11	6 AX470626	0.818182
c2770	9	45	11	6 AX624031	0.818182
c2771	9	45	11	6 AX631452	0.818182
c 373	10.4	52	13	6 AR002206	0.8
c10210	8	40	10	6 AR162919	0.8
c10211	8	40	10	6 AX096928	0.8
10212	8	40	10	6 AX152540	0.8
c10213	8	40	10	6 AX152940	0.8
c10214	8	40	10	6 AX301376	0.8
c10215	8	40	10	6 BD166804	0.8
c10216	8	40	10	6 I54931	0.8
c35354	7	35	9	6 AX318479	0.777778
35355	7	35	9	6 AX318480	0.777778
c35356	7	35	9	6 AX337949	0.777778
35357	7	35	9	6 AX337950	0.777778
c35358	7	35	9	6 AX337955	0.777778
35359	7	35	9	6 AX337956	0.777778
35360	7	35	9	6 AX668672	0.777778
35361	7	35	9	6 AX668673	0.777778
35362	7	35	9	6 AX668723	0.777778
35363	7	35	9	6 AX668724	0.777778
35364	7	35	9	6 AX668737	0.777778
35365	7	35	9	6 AX668738	0.777778
35366	7	35	9	6 AX668757	0.777778
35367	7	35	9	6 AX668795	0.777778
6002	8.4	42	11	6 AX099091	0.763636
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c6006	8.4	42	11	6 AX626928	0.763636
6007	8.4	42	11	6 AX627689	0.763636
c6008	8.4	42	11	6 AX627862	0.763636
c6009	8.4	42	11	6 AX629442	0.763636

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 14:14:22 ; Search time 185 Seconds
(without alignments)
291.831 Million cell updates/sec

Title: US-10-008-789-22

Perfect score: 20

Sequence: 1 gtttcaggagccgtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2100800

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65000 summaries

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4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:
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7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:
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 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*

 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Score/Length
No.	Score	Match	Length	DB ID	
c 934	10	50	10	21 AAZ82409	1
c13763	8	40	8	17 AAT09422	1
13764	8	40	8	17 AAT09561	1
3773	9	45	10	21 AAZ78197	0.9
3774	9	45	10	21 AAZ82165	0.9
3775	9	45	10	22 AAS57281	0.9
3776	9	45	10	22 AAH63996	0.9
3777	9	45	10	24 ABV73322	0.9
c3778	9	45	10	25 AAD47781	0.9
c13765	8	40	9	21 AAZ65526	0.888889
48636	7	35	8	17 AAT09588	0.875
c48637	7	35	8	17 AAT09371	0.875
c48638	7	35	8	17 AAT09466	0.875
c48639	7	35	8	17 AAT09425	0.875
48640	7	35	8	17 AAT09562	0.875
48641	7	35	8	17 AAT09544	0.875
48642	7	35	8	20 AAX78349	0.875
c48643	7	35	8	20 AAX29509	0.875
48644	7	35	8	21 AAA80773	0.875
c48645	7	35	8	21 AAA81033	0.875
c48646	7	35	8	21 AAA81034	0.875
c2089	9.4	47	11	24 ABV62975	0.854545
2090	9.4	47	11	24 ABV69534	0.854545
c2091	9.4	47	11	24 ABV70396	0.854545
7880	8.4	42	10	21 AAA56517	0.84
7881	8.4	42	10	21 AAA14247	0.84
c7882	8.4	42	10	21 AAZ78376	0.84
c7883	8.4	42	10	21 AAZ81654	0.84
7884	8.4	42	10	21 AAZ82050	0.84
7885	8.4	42	10	21 AAZ83201	0.84
7886	8.4	42	10	21 AAZ84054	0.84
c7887	8.4	42	10	21 AAZ84542	0.84
7888	8.4	42	10	21 AAZ85030	0.84

7889	8.4	42	10	21	AAZ85257	0.84
7890	8.4	42	10	21	AAZ85646	0.84
c7891	8.4	42	10	21	AAZ85771	0.84
7892	8.4	42	10	22	AAH63939	0.84
7893	8.4	42	10	22	AAH63940	0.84
7894	8.4	42	10	22	AAH20558	0.84
7895	8.4	42	10	22	AAH32842	0.84
7896	8.4	42	10	22	AAF75023	0.84
c7897	8.4	42	10	22	AAF40219	0.84
7898	8.4	42	10	22	AAF42414	0.84
c7899	8.4	42	10	24	AAL48143	0.84
7900	8.4	42	10	24	ABK81799	0.84
7901	8.4	42	10	24	AAS98841	0.84
7902	8.4	42	10	24	AAD25027	0.84
7903	8.4	42	10	24	ABL42775	0.84
7904	8.4	42	10	25	ABT14329	0.84
935	10	50	12	21	AAA52398	0.833333
27854	7.4	37	9	20	AAX54701	0.822222
27855	7.4	37	9	21	AAF20270	0.822222
27856	7.4	37	9	21	AAA34148	0.822222
27857	7.4	37	9	24	ABQ71834	0.822222
27858	7.4	37	9	24	ABQ71835	0.822222
27859	7.4	37	9	24	ABQ71836	0.822222
27860	7.4	37	9	24	ABQ71837	0.822222
c3779	9	45	11	22	AAS01932	0.818182
3780	9	45	11	22	AAS01933	0.818182
c3781	9	45	11	24	ABV63286	0.818182
c3782	9	45	11	24	ABV70707	0.818182
c3783	9	45	11	24	ABQ86448	0.818182
490	10.4	52	13	18	AAV11102	0.8
c13766	8	40	10	16	AAX32621	0.8
c13767	8	40	10	21	AAZ80768	0.8
c13768	8	40	10	21	AAZ82243	0.8
13769	8	40	10	21	AAZ82499	0.8
13770	8	40	10	21	AAZ83879	0.8
c13771	8	40	10	21	AAZ85236	0.8
13772	8	40	10	21	AAZ85403	0.8
13773	8	40	10	21	AAZ85929	0.8
13774	8	40	10	22	AAH63615	0.8
c13775	8	40	10	22	AAH64015	0.8
c13776	8	40	10	22	AAF97341	0.8
c13777	8	40	10	22	AAF37906	0.8
c13778	8	40	10	22	AAF42841	0.8
c13779	8	40	10	24	AAD44471	0.8
c13780	8	40	10	24	ABV84539	0.8
13781	8	40	10	24	ABT05343	0.8
c13782	8	40	10	24	ABK96539	0.8
c13783	8	40	10	24	ABK85687	0.8
13784	8	40	10	24	ABA98387	0.8

13785	8	40	10	24 ABK70549	0.8
c13786	8	40	10	24 ABL52211	0.8
c13787	8	40	10	24 ABL52257	0.8
c13788	8	40	10	24 ABK23463	0.8
13789	8	40	10	24 AAD26187	0.8
13790	8	40	10	24 AAS19975	0.8
13791	8	40	10	24 ABL39540	0.8
13792	8	40	10	25 ABT14248	0.8
c 54	11.8	59	15	22 AAF50238	0.786667
55	11.8	59	15	24 AAS98729	0.786667
48647	7	35	9	14 AAQ37100	0.777778
c48648	7	35	9	17 AAT27993	0.777778
48649	7	35	9	24 ABQ71823	0.777778
48650	7	35	9	24 ABQ71824	0.777778
48651	7	35	9	24 ABQ71874	0.777778
48652	7	35	9	24 ABQ71875	0.777778
48653	7	35	9	24 ABQ71888	0.777778
48654	7	35	9	24 ABQ71889	0.777778
48655	7	35	9	24 ABQ71908	0.777778
48656	7	35	9	24 ABQ71946	0.777778
c48657	7	35	9	25 AAD53774	0.777778
c7905	8.4	42	11	14 AAQ51997	0.763636
7906	8.4	42	11	22 AAS02884	0.763636
c7907	8.4	42	11	22 AAS02885	0.763636
c7908	8.4	42	11	24 ABV66076	0.763636
c7909	8.4	42	11	24 ABV66183	0.763636
7910	8.4	42	11	24 ABV66944	0.763636
c7911	8.4	42	11	24 ABV67117	0.763636
c7912	8.4	42	11	24 ABV68697	0.763636
c7913	8.4	42	11	24 ABQ87254	0.763636
c7914	8.4	42	11	24 ABL51577	0.763636
3784	9	45	12	24 ABK72572	0.75

GenConversion 5.1.6
Copyrig(c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic searusing sw model
Run on: November 5, 2003 15:28:18 ; Search time
(without alignments)
176.6 Million cell updates/sec

Title: US-10-008-789-22

Perfect score: 20

Sequence 1 gtttcagg 20

Scoring table: IDENTITY_NUC

Gapopen 10 , Gape 1

Searched 6E+05 seqs, 2E+08 residues

Total number of hits satisfied chosen parameters 544510

MinimumDB seq length: 8

MaximumDB seq length: 30

Post-prod MinimumMatch 0%

MaximumMatch 100%

Listing first 65000 summaries

Database Issued_Patents_NA:*

1:00 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2:00 /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3:00 /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4:00 /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5:00 /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6:00 /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the num of results predicted by
score greater than or equal to the score
and is derived by analysis of the total score

SUMMARIES

%

Result	Query					Score/Length
No.	Score	Match	Length	DB	ID	
19282	7	35	8	3	US-08-859-954-86	0.875
c19283	7	35	8	3	US-08-859-954-346	0.875
c19284	7	35	8	3	US-08-859-954-347	0.875

11288	7.4	37	9	1 US-08-566-037A-21	0.822222
c 232	10.4	52	13	1 US-08-259-148A-60	0.8
c 233	10.4	52	13	2 US-07-876-941A-76	0.8
c5667	8	40	10	1 US-08-202-927-21	0.8
c5668	8	40	10	3 US-09-424-518-1	0.8
c5669	8	40	10	5 PCT-US95-02419-21	0.8
37415	6.4	32	8	1 US-08-232-144-10	0.8
37416	6.4	32	8	2 US-08-480-473B-32	0.8
c37417	6.4	32	8	2 US-08-480-473B-34	0.8
37418	6.4	32	8	3 US-08-915-213-32	0.8
c37419	6.4	32	8	3 US-08-915-213-34	0.8
37420	6.4	32	8	3 US-08-646-301A-10	0.8
37421	6.4	32	8	3 US-09-235-217-32	0.8
c37422	6.4	32	8	3 US-09-235-217-34	0.8
c37423	6.4	32	8	3 US-09-544-713-4	0.8
37424	6.4	32	8	5 PCT-US96-10251-32	0.8
c37425	6.4	32	8	5 PCT-US96-10251-34	0.8
37426	6.4	32	8	6 5179003-1	0.8
c37427	6.4	32	8	6 5179003-1	0.8
c19285	7	35	9	1 US-08-331-398A-37	0.777778
c19286	7	35	9	2 US-08-331-397B-37	0.777778
c19287	7	35	9	2 US-08-759-804A-37	0.777778
c19288	7	35	9	3 US-09-227-693-37	0.777778
c19289	7	35	9	4 US-09-528-760A-18	0.777778
19290	7	35	9	4 US-09-528-760A-19	0.777778
c19291	7	35	9	4 US-09-397-992A-32	0.777778
19292	7	35	9	4 US-09-397-992A-33	0.777778
c19293	7	35	9	4 US-09-526-416-3	0.777778
19294	7	35	9	4 US-09-526-416-4	0.777778
c19295	7	35	9	4 US-09-472-130A-13	0.777778
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c19299	7	35	9	4 US-09-951-843-18	0.777778
19300	7	35	9	4 US-09-951-843-19	0.777778
60723	6	30	8	2 US-08-574-586-6	0.75
c60724	6	30	8	2 US-08-593-345B-15	0.75
60725	6	30	8	2 US-08-480-473B-31	0.75
60726	6	30	8	3 US-09-069-434-6	0.75
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60730	6	30	8	3 US-08-859-954-85	0.75
60731	6	30	8	3 US-08-859-954-87	0.75
c60732	6	30	8	3 US-08-859-954-95	0.75
60733	6	30	8	3 US-08-859-954-338	0.75
c60734	6	30	8	3 US-08-859-954-348	0.75
c60735	6	30	8	3 US-08-859-954-510	0.75
60736	6	30	8	3 US-09-235-217-31	0.75

60737 6 30 8 5 PCT-US96-10251-31 0.75

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 15:30:03 ; Search time 177 Seconds
(without alignments)
360.560 Million cell updates/sec

Title: US-10-008-789-22

Perfect score: 20

Sequence: 1 gcttcaggagcccggtgcgg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 932664

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65000 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Score/Length
No.	Score	Match	Length	DB	ID	
1	20	100	20	14	US-10-008-789-22	1
2877	9	45	10	12	US-10-330-627-836	0.9
2878	9	45	10	13	US-10-033-145-625	0.9
6122	8.4	42	10	12	US-10-330-627-779	0.84
6123	8.4	42	10	12	US-10-330-627-780	0.84
c6124	8.4	42	10	13	US-10-033-145-804	0.84
21115	7.4	37	9	9	US-09-989-789-2132	0.822222
21116	7.4	37	9	9	US-09-989-789-2133	0.822222
21117	7.4	37	9	9	US-09-989-789-2134	0.822222
21118	7.4	37	9	9	US-09-989-789-2135	0.822222
21119	7.4	37	9	11	US-09-990-186-2132	0.822222
21120	7.4	37	9	11	US-09-990-186-2133	0.822222
21121	7.4	37	9	11	US-09-990-186-2134	0.822222
21122	7.4	37	9	11	US-09-990-186-2135	0.822222
21123	7.4	37	9	11	US-09-989-994-2132	0.822222
21124	7.4	37	9	11	US-09-989-994-2133	0.822222
21125	7.4	37	9	11	US-09-989-994-2134	0.822222
21126	7.4	37	9	11	US-09-989-994-2135	0.822222
10659	8	40	10	12	US-10-330-627-455	0.8
c10660	8	40	10	12	US-10-330-627-855	0.8
c36258	7	35	9	9	US-09-842-746-1	0.777778
36259	7	35	9	9	US-09-842-746-2	0.777778
36260	7	35	9	9	US-09-989-789-2121	0.777778
36261	7	35	9	9	US-09-989-789-2122	0.777778
36262	7	35	9	9	US-09-989-789-2172	0.777778
36263	7	35	9	9	US-09-989-789-2173	0.777778
36264	7	35	9	9	US-09-989-789-2186	0.777778
36265	7	35	9	9	US-09-989-789-2187	0.777778
36266	7	35	9	9	US-09-989-789-2206	0.777778
36267	7	35	9	9	US-09-989-789-2244	0.777778
c36268	7	35	9	9	US-09-873-134-5	0.777778
36269	7	35	9	9	US-09-873-134-6	0.777778
c36270	7	35	9	10	US-09-951-843-18	0.777778
36271	7	35	9	10	US-09-951-843-19	0.777778
c36272	7	35	9	11	US-09-971-843-32	0.777778
36273	7	35	9	11	US-09-971-843-33	0.777778
36274	7	35	9	11	US-09-990-186-2121	0.777778
36275	7	35	9	11	US-09-990-186-2122	0.777778
36276	7	35	9	11	US-09-990-186-2172	0.777778
36277	7	35	9	11	US-09-990-186-2173	0.777778
36278	7	35	9	11	US-09-990-186-2186	0.777778

36279	7	35	9	11	US-09-990-186-2187	0.777778
36280	7	35	9	11	US-09-990-186-2206	0.777778
36281	7	35	9	11	US-09-990-186-2244	0.777778
36282	7	35	9	11	US-09-989-994-2121	0.777778
36283	7	35	9	11	US-09-989-994-2122	0.777778
36284	7	35	9	11	US-09-989-994-2172	0.777778
36285	7	35	9	11	US-09-989-994-2173	0.777778
36286	7	35	9	11	US-09-989-994-2186	0.777778
36287	7	35	9	11	US-09-989-994-2187	0.777778
36288	7	35	9	11	US-09-989-994-2206	0.777778
36289	7	35	9	11	US-09-989-994-2244	0.777778
c36290	7	35	9	12	US-10-358-619-18	0.777778
36291	7	35	9	12	US-10-358-619-19	0.777778
c36292	7	35	9	12	US-09-873-135-5	0.777778
36293	7	35	9	12	US-09-873-135-6	0.777778
c36294	7	35	9	12	US-10-124-090-5	0.777778
36295	7	35	9	12	US-10-124-090-6	0.777778
c36296	7	35	9	12	US-10-277-494-134	0.777778
36297	7	35	9	12	US-10-277-494-212	0.777778
c36298	7	35	9	14	US-10-152-363A-57	0.777778
36299	7	35	9	14	US-10-152-363A-58	0.777778
95	11.4	57	15	12	US-10-133-779-170	0.76

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 14:56:18 ; Search time 1628 Seconds
(without alignments)
298.581 Million cell updates/sec

Title: US-10-008-789-22

Perfect score: 20

Sequence: 1 gcttcaggagcccggtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33250

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65000 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:
 21: em_gss_fun:
 22: em_gss_mam:
 23: em_gss_mus:
 24: em_gss_pro:
 25: em_gss_rod:
 26: em_gss_phg:
 27: em_gss_vrl:
 28: gb_gss1:
 29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Score/Length
No.	Score	Match	Length	DB	ID	
c 738	7.4	37	10	12	BM393918	0.74
c 739	7.4	37	10	14	CA794390	0.74
c 455	7.8	39	11	12	BM395371	0.709091
c 29	9.4	47	15	12	BM395189	0.626667
239	8.2	41	14	28	BH169716	0.585714
4433	5.8	29	10	12	BM396043	0.58
c 740	7.4	37	13	12	BM394028	0.569231
c 82	8.8	44	16	12	BM395110	0.55
8	10.2	51	19	12	BM397569	0.536842
741	7.4	37	14	12	BM392794	0.528571
742	7.4	37	14	12	BM394089	0.528571
c4434	5.8	29	11	13	BQ591023	0.527273
c7902	5.2	26	10	12	BM396011	0.52
c7903	5.2	26	10	12	BM398849	0.52
83	8.8	44	17	12	BM397301	0.517647
938	7.2	36	14	12	BM398539	0.514286
240	8.2	41	16	12	BM397868	0.5125
39	9.2	46	18	12	BM397051	0.511111
9353	5	25	10	14	CA794390	0.5
20273	4	20	8	14	CA794554	0.5
30	9.4	47	19	9	AA912825	0.494737
743	7.4	37	15	12	BM395188	0.493333
c2280	6.4	32	13	12	BM395265	0.492308
2281	6.4	32	13	12	BM396800	0.492308
c6154	5.4	27	11	12	BM395068	0.490909
c6155	5.4	27	11	12	BM395228	0.490909
6156	5.4	27	11	13	BQ594565	0.490909
6157	5.4	27	11	28	BH213431	0.490909
c1609	6.8	34	14	28	BH169716	0.485714